



#6

SEQUENCE LISTING

<110> MURRAY, RICHARD

<120> Novel Methods of Diagnosis of Angiogenesis,
Compositons, and Methods of Screening for Angiogenesis
Modulators

<130> A-68110-1/DJB/RMS/DCF

<140> US 09/637,977

<141> 2000-08-11

<150> US 60/148,425

<151> 1999-08-11

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 1237

<212> DNA

<213> Homo sapiens

<400> 1

```
gttcgcgcgc gccgcgcgcgc ccacctggag ttttttcaga ctccagattt cctgttcaac 60
cacgaggagt ccagagagga aacgcggagc ggagacaaca gtacctgacg cctctttcag 120
cccgggatcg cccagcagg gatgggcgac aagatctggc tgcccttccc cgtgtctcctt 180
ctggcgcgtc tgccctcggg gctgctgcct ggggcggcgc gcttcacacc ttcctctgat 240
agcgacttca cctttaccct tccgcgcgcgc cagaaggagt gcttctacca gcccatgccc 300
ctgaaggcct cgctggagat cgagtaccaa gtttttagatg gagcaggatt agatattgat 360
ttccatcttg cctctccaga aggcaaaacc ttagtttttg aacaaagaaa atcagatgga 420
gttcacactg tagagactga agttggtgat tacatgttct gctttgacaa tacattcagc 480
accatttctg agaagggtgat tttctttgaa ttaatcctgg ataatatggg agaacaggca 540
caagaacaag aagattggaa gaaatatatt actggcacag atatattgga tatgaaactg 600
gaagacatcc tggaatccat caacagcatc aagtcagac taagcaaaag tgggcacata 660
caaactctgc ttagagcatt tgaagctcgt gatcgaaaca tacaagaaag caactttgat 720
agagtcaatt tctggtctat ggtaatttta gtggtcatgg tgggtggtgc agccattcaa 780
gtttatatgc tgaagagtct gtttgaagat aagaggaaaa gtagaactta aaactccaaa 840
ctagagtacg taacattgaa aaatgaggca taaaatgca ataaactggt acagtcaaga 900
ccattaatgg tcttctccaa aatattttga gatataaaag taggaaacag gtataatttt 960
aatgtgaaaa ttaagtcttc actttctgtg caagtaatcc tgctgatcca gttgtactta 1020
agtgtgtaac aggaatattt tgcagaatat aggtttaact gaatgaagcc atattaataa 1080
ctgcattttc ctaactttga aaaattttgc aaatgtctta ggtgatttaa ataaatgagt 1140
attgggccta aatgcaacac cagtctgttt tgaacaggtt ctattacca gaactttttt 1200
gtaaatgcgc cagttacaaa ttaactgttg gaggtttt 1237
```

<210> 2
 <211> 690
 <212> DNA
 <213> Homo sapiens

<400> 2
 atgggcgaca agatctggct gcccttcccc gtgctccttc tggccgctct gcctccggtg 60
 ctgctgcctg gggcgggcgg cttcacacct tccctcgata gcgacttcac ctttaccctt 120
 cccgcgggcc agaaggagtg cttctaccag cccatgcccc tgaaggcctc gctggagatc 180
 gagtaccaag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa 240
 ggcaaacct tagtttttga acaaagaaaa tcagatggag ttcacactgt agagactgaa 300
 gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaagggtgatt 360
 ttctttgaat taatcctgga taatatggga gaacaggcac aagaacaaga agattggaag 420
 aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc 480
 aacagcatca agtcagact aagcaaaagt gggcacatac aaactctgct tagagcattt 540
 gaagctcgtg atcgaaacat acaagaaagc aactttgata gagtcaattt ctggtctatg 600
 gttaatttag tggatcatgg ggtggtgtca gccattcaag tttatatgct gaagagtctg 660
 tttgaagata agaggaaaa tagaacttaa 690

<210> 3
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 3
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 1 5 10 15
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 20 25 30
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35 40 45
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50 55 60
 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 65 70 75 80
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 85 90 95
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 100 105 110

Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
115 120 125

Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
130 135 140

Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
145 150 155 160

Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Thr Leu
165 170 175

Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
180 185 190

Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
195 200 205

Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
210 215 220

Arg Lys Ser Arg Thr
225

<210> 4
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 4
Cys Met Leu Lys Ser Leu Phe Glu Asp Lys Arg Lys Ser Arg Thr
1 5 10 15

<210> 5
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

<400> 5
Cys Ala Gly Phe Thr Pro Ser Leu Asp Ser Asp Phe Thr Phe Thr

1

5

10

15

<210> 6

<211> 905

<212> DNA

<213> Homo sapiens

<400> 6

taaaaatcga gctgagatga tagatttcaa tatccggatc aaaaatgtga caagaagtga 60
 tgcggggaaa tatcgttgtg aagttagtgc cccatctgag caaggccaaa acctggaaga 120
 ggatacagtc actctggaag tattagtggc tccagcagtt ccatcatgtg aagtaccctc 180
 ttctgctctg agtggaactg tggatatctt acgatgtcaa gacaaagaag ggaatccagc 240
 tcttgaatac acatggttta aggatggcat ccgtttgcta gaaaatccca gacttggtc 300
 ccaaagcacc aacagctcat acacaatgaa tacaaaaact ggaactctgc aatttaatac 360
 tgtttccaaa ctggacactg gagaatatct ctgtgaagcc cgcaattctg ttggatatcg 420
 caggtgtcct gggaaacgaa tgcaagtaga tgatctcaac ataagtggca tcatagcagc 480
 cgtagtagtt gtggccttag tgatttcgtt ttgtggcctt ggtgtatgct atgctcagag 540
 gaaaggctac ttttcaaaag aaacctcctt ccagaagagt aattcttcat ctaaagccac 600
 gacaatgagt gaaaatgatt tcaagcacac aaaatccttt ataatttaaa gactccactt 660
 tagagataca ccaaagccac cgttggtaca caagttatta aactattata aaactctgct 720
 ttgtccgaca ttgtcaaaga ggtacacgag gaaatggaat tggattttca ttttaatttt 780
 catgactact aactcacctg aacttgctat tttaaacaaa tagttctgtc gacacctaaa 840
 atataatctg gcttcttgtg tctggactaa gttaaaagaa ttaaaatact ttgtaatgtc 900
 aaaaa 905

<210> 7

<211> 215

<212> PRT

<213> Homo sapiens

<400> 7

Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile Lys Asn Val
 1 5 10 15
 Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser Ala Pro Ser
 20 25 30
 Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu Glu Val Leu
 35 40 45
 Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser Ala Leu Ser
 50 55 60
 Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala
 65 70 75 80

Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu Glu Asn Pro
85 90 95

Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys
100 105 110

Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp Thr Gly Glu
115 120 125

Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg Cys Pro Gly
130 135 140

Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala
145 150 155 160

Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu Gly Val Cys
165 170 175

Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser Phe Gln Lys
180 185 190

Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys
195 200 205

His Thr Lys Ser Phe Ile Ile
210 215

<210> 8
<211> 15
<212> PRT
<213> Homo sapiens

<400> 8
Cys Ala Thr Thr Met Ser Glu Asn Asp Phe Lys His Thr Lys Ser
1 5 10 15

<210> 9
<211> 14
<212> PRT
<213> Homo sapiens

<400> 9
Arg Cys Gln Asp Lys Glu Gly Asn Pro Ala Pro Glu Tyr Thr
1 5 10

<210> 10
 <211> 2757
 <212> DNA
 <213> Homo sapiens

<400> 10

```
tctaaagggtc ggggggcagca gcaagatgcg aagccgagcc gtacagatcc cggtctctccg 60
aacgcaactt cgccctgctt gagcgaggct gcggtttccg aggccctctc cagccaagga 120
aaagctacac aaaaagcctg gatcactcat cgaaccaccc ctgaagccag tgaaggctct 180
ctcgctcgc cctctagcgt tcgtctggag tagcgccacc cgggttctt ggggacacag 240
ggttggcacc atggggccca ccagcgctcc gctggtcaag gccacccgca gctcggctct 300
tgactacgtc aactatgata tcatcgctcc gcattacaac tacacgggaa agctgaatat 360
cagcgccggac aaggagaaca gcattaaact gacctcgggt gtgttcattc tcatctgctg 420
ctttatcacc ctggagaaca tctttgtctt gctgaccatt tggaaaacca agaaattcca 480
ccgacccatg tactatttta ttggcaatct ggccctctca gacctgttgg caggagtagc 540
ctacacagct aacctgctct tgtctggggc caccacctac aagctcactc ccgcccagtg 600
gtttctgcgg gaagggagta tgtttgtggc cctgtcagcc tccgtgttca gtctcctcgc 660
catcgccatt gagcgctata tcacaatgct gaaaatgaaa ctccacaacg ggagcaataa 720
cttccgcctc ttcctgctaa tcagcgctg ctgggtcacc tccctcatcc tgggtggcct 780
gcctatcatg ggctggaact gcacagtgct gctgtccagc tgetccaccg tgetgccgct 840
ctaccacaag cactatatcc tcttctgcac cacggtcttc actctgcttc tgetctccat 900
cgtcattctg tactgcagaa tctactcctt ggtcaggact cggagcccgc cgtgacggt 960
ccgcaagaac atttccaagg ccagccgcag ctctgagaat gtggcgctgc tcaagaccgt 1020
aattatcgct ctgagcgtct tcatcgctct ctgggcaccg ctcttcatcc tgetcctgct 1080
ggatgtgggg tgcaaggtga agacctgtga catcctcttc agagcggagt acttctcgtt 1140
gttagctgtg ctcaactccg gcaccaaccc catcatttac actctgacca acaaggagat 1200
gcgtcggggc ttcacccgga tcatgtcctg ctgcaagtgc ccgagcggag actctgctgg 1260
caaattcaag cgacccatca tcgccggcat ggaattcagc cgcagcaaat cggacaattc 1320
ctccaccccc cagaaagacg aaggggacaa ccagagacc attatgtctt ctggaaacgt 1380
caactcttct tctagaact ggaagctgtc caccacccg aagcgctctt tacttggctg 1440
ctggccaccc cagtgttttg aaaaaaatct ctgggcttcg actgctgcca gggaggagct 1500
gctgcaagcc agagggagga agggggagaa tacgaacagc ctgggtggtgt cgggtgttgg 1560
tgggtagagt tagttcctgt gaacaatgca ctgggaaggg tggagatcag gtcccggcct 1620
ggaatatata ttctaccccc ctggagcttt gattttgcac tgagccaaag gtctagcatt 1680
gtcaagctcc taaagggttc atttggcccc tctcaaaga ctaatgtccc catgtgaaag 1740
cgtctctttg tctggagctt tgaggagatg ttttcttca ctttagtttc aaaccaagt 1800
gagtgtgtgc acttctgctt ctttagggat gccctgtaca tccacaccc caccctccct 1860
tcccttcata cccctcctca acgttctttt actttatact ttaactacct gagagttagc 1920
agagctgggg ttgtggaatg atcgatcatc tatagcaaat aggctatgtt gagtacgtag 1980
gctgtgggaa gatgaagatg gtttggagggt gtaaaacaat gtccttcgct gaggccaaag 2040
tttccatgta agcgggatcc gttttttgga atttggttga agtcactttg atttctttaa 2100
aaaacatctt ttcaatgaaa tgtgttacca tttcatatcc attgaagccg aaatctgcat 2160
aaggaagccc actttatcta aatgatatta gccaggatcc ttggtgtcct aggagaaaca 2220
gacaagcaaa acaaagtga aaccgaatgg attaactttt gcaaaccaag ggagatttct 2280
tagcaaatga gtctaacaaa tatgacatcc gtctttccca cttttgttga tgtttatttc 2340
agaatcttgt gtgattcatt tcaagcaaca acatgttgta ttttgttgtg ttaaaagtac 2400
ttttcttgat ttttgaatgt atttgtttca ggaagaagtc attttatgga tttttctaac 2460
ccgtgttaac ttttctagaa tccaccctct tgtgccctta agcattactt taactggtag 2520
```

ggaacgccag aacttttaag tccagctatt cattagatag taattgaaga tatgtataaa 2580
tattacaaag aataaaaata tattactgtc tcttttagtat ggttttcagt gcaattaaac 2640
cgagagatgt cttgtttttt taaaaagaat agtatttaat aggtttctga cttttgtgga 2700
tcattttgca catagcttta tcaactttta aacattaata aactgatttt tttaaag 2757

<210> 11

<211> 1146

<212> DNA

<213> Homo sapiens

<400> 11

atggggccca ccagcgcccc gctgggtcaag gccaccgcga gctcggtctc tgactacgtc 60
aactatgata tcacggtccg gcattacaac tacacgggaa agctgaatat cagcgcggac 120
aaggagaaca gcattaaact gacctcggtg gtgttcattc tcactctgtg ctttatcacc 180
ctggagaaca tctttgtctt gctgaccatt tggaaaacca agaaattcca ccgacccatg 240
tactatttta ttggcaatct ggccctctca gacctgttgg caggagtagc ctacacagct 300
aacctgctct tgtctggggc caccacctac aagctcactc ccgcccagtg gtttctgogg 360
gaagggagta tgtttgtggc cctgtcagcc tccgtgttca gtctcctcgc catcgccatt 420
gagcgctata tcacaatgct gaaaatgaaa ctccacaacg ggagcaataa cttccgcctc 480
ttcctgctaa tcagcgctcg ctgggtcacc tccctcatcc tgggtggcct gcctatcatg 540
ggctggaact gcacagtgcc gctgtccagc tgctccaccg tgctgccgct ctaccacaag 600
cactatatcc tcttctgcac caccgtcttc actctgcttc tgctctccat cgtcattctg 660
tactgcagaa tctactcctt ggtcaggact cggagccgcc gcctgacgtt ccgcaagaac 720
atttccaagg ccagccgcag ctctgagaat gtggcgctgc tcaagaccgt aattatcgtc 780
ctgagcgctc tcacgctcg ctgggcaccg ctcttcatcc tgctcctgct ggatgtgggc 840
tgcaagggtga agacctgtga catcctcttc agagcggagt acttctggt gttagctgtg 900
ctcaactccg gcaccaaccc catcatttac actctgacca acaaggagat gcgtcggggc 960
ttcatccgga tcatgtcctg ctgcaagtgc ccgagcggag actctgctgg caaattcaag 1020
cgacccatca tcgccggcat ggaattcagc cgcagcaaat cggacaattc ctcccacccc 1080
cagaaagacg aaggggacaa ccagagacc attatgtctt ctggaaacgt caactcttct 1140
tcctag 1146

<210> 12

<211> 381

<212> PRT

<213> Homo sapiens

<400> 12

Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Val
1 5 10 15
Ser Asp Tyr Val Asn Tyr Asp Ile Ile Val Arg His Tyr Asn Tyr Thr
20 25 30
Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr
35 40 45

Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile
 50 55 60

Phe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met
 65 70 75 80

Tyr Tyr Phe Ile Gly Asn Leu Ala Leu Ser Asp Leu Leu Ala Gly Val
 85 90 95

Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu
 100 105 110

Thr Pro Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu
 115 120 125

Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile
 130 135 140

Thr Met Leu Lys Met Lys Leu His Asn Gly Ser Asn Asn Phe Arg Leu
 145 150 155 160

Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly
 165 170 175

Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser
 180 185 190

Thr Val Leu Pro Leu Tyr His Lys His Tyr Ile Leu Phe Cys Thr Thr
 195 200 205

Val Phe Thr Leu Leu Leu Leu Ser Ile Val Ile Leu Tyr Cys Arg Ile
 210 215 220

Tyr Ser Leu Val Arg Thr Arg Ser Arg Arg Leu Thr Phe Arg Lys Asn
 225 230 235 240

Ile Ser Lys Ala Ser Arg Ser Ser Glu Asn Val Ala Leu Leu Lys Thr
 245 250 255

Val Ile Ile Val Leu Ser Val Phe Ile Ala Cys Trp Ala Pro Leu Phe
 260 265 270

Ile Leu Leu Leu Leu Asp Val Gly Cys Lys Val Lys Thr Cys Asp Ile
 275 280 285

Leu Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser Gly
 290 295 300

Thr Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg Ala
305 310 315 320

Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Pro Ser Gly Asp Ser Ala
325 330 335

Gly Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg Ser
340 345 350

Lys Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn Pro
355 360 365

Glu Thr Ile Met Ser Ser Gly Asn Val Asn Ser Ser Ser
370 375 380

<210> 13

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 13

Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Cys
1 5 10 15

<210> 14

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 14

Cys Thr Thr Tyr Lys Leu Thr Pro Ala Gln Trp Phe Leu Arg Glu
1 5 10 15

<210> 15

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 15

Cys Asn Pro Ile Ile Tyr Thr Leu Thr Asn Lys Glu Met Arg Arg
1 5 10 15

<210> 16

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 16

Lys Leu Asn Ile Gly Ala Glu Lys Asp His Gly Ile Lys Leu Cys
1 5 10 15

<210> 17

<211> 4204

<212> DNA

<213> Homo sapiens

<400> 17

caggacaggg aagagcgggc gctatgggga gccggacgcc agagtcccct ctccacgccg 60
tgcagctgcg ctggggcccc cggcgccgac ccccgctcgt gccgctgctg ttgctgctcg 120
tgccgcccgc acccagggtc gggggcttca acttagacgc ggaggcccca gcagtactct 180
cggggccccc gggctccttc ttcggtattct cagtggagtt ttaccggccg ggaacagacg 240
gggtcagtggt gctggtggga gcacccaagg ctaataccag ccagccagga gtgctgcagg 300
gtggtgctgt ctacctctgt ccttgggggt ccagccccac acagtgcacc cccattgaat 360
ttgacagcaa aggtctctcg ctctggaggt cctcactgtc cagctcagag ggagaggagc 420
ctgtggagta caagtccttg cagtgggttc gggcaacagt tcgagcccat ggctcctcca 480
tcttggcatg cgctccactg tacagctggc gcacagagaa ggagccactg agcgaccccg 540
tgggcacctg ctacctctcc acagataact tcacccgaat tctggagtat gcacctgcc 600
gctcagattt cagctgggca gcaggacagg gttactgcca aggaggcttc agtgccgagt 660
tcaccaagac tggccgtgtg gtttttaggt gaccaggaag ctatttcttg caaggccaga 720
tctgtctgct cactcaggag cagattgcag aatcttatta ccccgagtac ctgatcaacc 780
tggttcaggg gcagctgcag actcgccagg ccagttccat ctatgatgac agctacctag 840
gatactctgt ggctgttggg gaattcagtg gtgatgacac agaagacttt gttgctgggt 900
tgcccaaagg gaacctcact tacggctatg tcaccatcct taatggctca gacattcgat 960
ccctctacaa cttctcaggg gaacagatgg cctcctactt tggctatgca gtggccgcca 1020
cagacgtcaa tggggacggg ctggatgact tgctggtggg ggcaccctg ctcatggatc 1080
ggaccctga cgggcggcct caggaggtgg gcagggtcta cgtctacctg cagcaccag 1140
ccggcataga gccacgccc acccttacct tctactggcca tgatgagttt ggccgatttg 1200
gcagctcctt gacccccctg ggggacctgg accaggatgg ctacaatgat gtggccatcg 1260

gggctccctt tgggtggggag acccagcagg gagtagtggt tgtatttcct gggggcccag 1320
 gagggctggg ctctaagcct tcccagggttc tgcagccctt gtgggcagcc agccacaccc 1380
 cagacttctt tggctctgcc cttcgaggag gccgagacct ggatggcaat ggatatcctg 1440
 atctgattgt ggggtccctt ggtgtggaca aggtgtggt atacaggggc cgcctcatcg 1500
 tgctcgttag tgccctccctc accatcttcc ccgccatgtt caaccagag gagcggagct 1560
 gcagcttaga ggggaacct gtggcctgca tcaaccttag cttctgcctc aatgcttctg 1620
 gaaaacacgt tgctgactcc attggtttca cagtggaaact tcagctggac tggcagaagc 1680
 agaagggagg ggtacggcgg gcactgttcc tggcctccag gcaggcaacc ctgacccaga 1740
 ccctgctcat ccagaatggg gctcgagagg attgcagaga gatgaagatc tacctcagga 1800
 acgagtcaga atttcgagac aaactctcgc cgattcacat cgctctcaac ttctccttgg 1860
 accccaagc ccagtgagc agccacggcc tcaggccagc cctacattat cagagcaaga 1920
 gccggataga ggacaaggct cagatcttgc tggactgtgg agaagacaac atctgtgtgc 1980
 ctgacctgca gctggaagtg tttggggagc agaaccatgt gtacctgggt gacaagaatg 2040
 ccctgaacct cactttccat gcccagaatg tgggtgaggg tggcgccctat gaggtgagc 2100
 ttccgggtcac cgcctccca gaggtgagc actcaggact cgtcagacac ccagggaact 2160
 tctccagcct gagctgtgac tactttgccg tgaaccagag ccgcctgctg gtgtgtgacc 2220
 tgggcaaccc catgaaggca ggagccagtc tgtgggggtg ccttcgggtt acagtccctc 2280
 atctccggga cactaagaaa accatccagt ttgacttcca gatcctcagc aagaatctca 2340
 acaactcgca aagcgacgtg gtttccttcc ggctctccgt ggaggctcag gcccaggtca 2400
 ccctgaacgg tgtctccaag cctgaggcag tgctattccc agtaagcgac tggcatcccc 2460
 gagaccagcc tcagaaggag gaggacctgg gacctgctgt ccacctgtc tatgagctca 2520
 tcaaccaagg cccagctcc attagccagg gtgtgctgga actcagctgt cccaggtc 2580
 tggaaggtca gcagctccta tatgtgacca gagttacggg actcaactgc accaccaatc 2640
 accccattaa cccaaagggc ctggagttgg atcccgaggg ttccctgcac caccagcaaa 2700
 aacgggaagc tccaagccgc agctctgctt cctcgggacc tcagatcctg aaatgcccg 2760
 aggtgagtg tttcaggctg cgtgtgagc tcgggcccct gcaccaacaa gagagccaaa 2820
 gtctgcagtt gcatttccga gtctgggcca agactttctt gcagcgggag caccagccat 2880
 ttagcctgca gtgtgaggct gtgtacaaag ccctgaagat gccctaccga atcctgcctc 2940
 ggcagctgcc ccaaaaagag cgtcaggtgg ccacagctgt gcaatggacc aaggcagaag 3000
 gcagctatgg cgtcccactg tggatcatca tctagccat cctgtttggc ctctgctcc 3060
 taggtctact catctacatc ctctacaagc ttggattctt caaacgctcc ctcccatatg 3120
 gcaccgccat ggaaaaagct cagctcaagc ctccagccac ctctgatgcc tgagtcctcc 3180
 caatttcaga ctccattcc tgaagaacca gtccccccac cctcattcta ctgaaaagga 3240
 ggggtctggg tacttcttga aggtgctgac ggccaggag aagctcctct cccagccca 3300
 gagacatact tgaaggcca gagccagggg ggtgaggagc tggggatccc tccccccat 3360
 gcactgtgaa ggaccttgt ttacacatac cctcttcatg gatgggggaa ctcatgcca 3420
 gggacagagg ccagcctcc ctgaagcctt tgcattttgg agagtttct gaaacaactg 3480
 gaaagataac taggaaatcc attcacagtt ctttgggcca gacatgccac aaggacttcc 3540
 tgctcagctc caacctgcaa agatctgtcc tcagccttgc cagagatcca aaagaagccc 3600
 ccagtaagaa cctggaactt ggggagttaa gacctggcag ctctggacag cccaccctg 3660
 gtgggccaac aaagaacact aactatgcat ggtgcccag gaccagctca ggacagatgc 3720
 cacaaggata gatgctggcc cagggccaga gccagctcc aaggggaatc agaactcaa 3780
 tggggccaga tccagcctgg ggtctggagt tgatctggaa ccagactca gacattggca 3840
 ccaatccagg cagatccagg actatatttg ggcctgctcc agacctgatc ctggaggccc 3900
 agttcacctt gatttaggag aagccaggaa tttcccagga cctgaagggg ccatgatggc 3960
 aacagatctg gaacctcagc ctggccagac acaggccctc cctgttcccc agagaaaggg 4020
 gagccactg tcctgggcct gcagaatttg ggttctgcct gccagctgca ctgatgctgc 4080
 ccctcatctc tctgccaac cttccctca ccttggcacc agacaccag gacttattta 4140

aactctgttg caagtgcaat aaatctgacc cagtgcacccc actgaccaga actagaaaaa 4200
 aaaa 4204

<210> 18
 <211> 1049
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Gly Ser Arg Thr Pro Glu Ser Pro Leu His Ala Val Gln Leu Arg
 1 5 10 15

Trp Gly Pro Arg Arg Arg Pro Pro Leu Val Pro Leu Leu Leu Leu Leu
 20 25 30

Val Pro Pro Pro Pro Arg Val Gly Gly Phe Asn Leu Asp Ala Glu Ala
 35 40 45

Pro Ala Val Leu Ser Gly Pro Pro Gly Ser Phe Phe Gly Phe Ser Val
 50 55 60

Glu Phe Tyr Arg Pro Gly Thr Asp Gly Val Ser Val Leu Val Gly Ala
 65 70 75 80

Pro Lys Ala Asn Thr Ser Gln Pro Gly Val Leu Gln Gly Gly Ala Val
 85 90 95

Tyr Leu Cys Pro Trp Gly Ala Ser Pro Thr Gln Cys Thr Pro Ile Glu
 100 105 110

Phe Asp Ser Lys Gly Ser Arg Leu Leu Glu Ser Ser Leu Ser Ser Ser
 115 120 125

Glu Gly Glu Glu Pro Val Glu Tyr Lys Ser Leu Gln Trp Phe Gly Ala
 130 135 140

Thr Val Arg Ala His Gly Ser Ser Ile Leu Ala Cys Ala Pro Leu Tyr
 145 150 155 160

Ser Trp Arg Thr Glu Lys Glu Pro Leu Ser Asp Pro Val Gly Thr Cys
 165 170 175

Tyr Leu Ser Thr Asp Asn Phe Thr Arg Ile Leu Glu Tyr Ala Pro Cys
 180 185 190

Arg Ser Asp Phe Ser Trp Ala Ala Gly Gln Gly Tyr Cys Gln Gly Gly
 195 200 205

Phe Ser Ala Glu Phe Thr Lys Thr Gly Arg Val Val Leu Gly Gly Pro
210 215 220
Gly Ser Tyr Phe Trp Gln Gly Gln Ile Leu Ser Ala Thr Gln Glu Gln
225 230 235 240
Ile Ala Glu Ser Tyr Tyr Pro Glu Tyr Leu Ile Asn Leu Val Gln Gly
245 250 255
Gln Leu Gln Thr Arg Gln Ala Ser Ser Ile Tyr Asp Asp Ser Tyr Leu
260 265 270
Gly Tyr Ser Val Ala Val Gly Glu Phe Ser Gly Asp Asp Thr Glu Asp
275 280 285
Phe Val Ala Gly Val Pro Lys Gly Asn Leu Thr Tyr Gly Tyr Val Thr
290 295 300
Ile Leu Asn Gly Ser Asp Ile Arg Ser Leu Tyr Asn Phe Ser Gly Glu
305 310 315 320
Gln Met Ala Ser Tyr Phe Gly Tyr Ala Val Ala Ala Thr Asp Val Asn
325 330 335
Gly Asp Gly Leu Asp Asp Leu Leu Val Gly Ala Pro Leu Leu Met Asp
340 345 350
Arg Thr Pro Asp Gly Arg Pro Gln Glu Val Gly Arg Val Tyr Val Tyr
355 360 365
Leu Gln His Pro Ala Gly Ile Glu Pro Thr Pro Thr Leu Thr Leu Thr
370 375 380
Gly His Asp Glu Phe Gly Arg Phe Gly Ser Ser Leu Thr Pro Leu Gly
385 390 395 400
Asp Leu Asp Gln Asp Gly Tyr Asn Asp Val Ala Ile Gly Ala Pro Phe
405 410 415
Gly Gly Glu Thr Gln Gln Gly Val Val Phe Val Phe Pro Gly Gly Pro
420 425 430
Gly Gly Leu Gly Ser Lys Pro Ser Gln Val Leu Gln Pro Leu Trp Ala
435 440 445
Ala Ser His Thr Pro Asp Phe Phe Gly Ser Ala Leu Arg Gly Gly Arg
450 455 460

Asp Leu Asp Gly Asn Gly Tyr Pro Asp Leu Ile Val Gly Ser Phe Gly
 465 470 475 480
 Val Asp Lys Ala Val Val Tyr Arg Gly Arg Pro Ile Val Ser Ala Ser
 485 490 495
 Ala Ser Leu Thr Ile Phe Pro Ala Met Phe Asn Pro Glu Glu Arg Ser
 500 505 510
 Cys Ser Leu Glu Gly Asn Pro Val Ala Cys Ile Asn Leu Ser Phe Cys
 515 520 525
 Leu Asn Ala Ser Gly Lys His Val Ala Asp Ser Ile Gly Phe Thr Val
 530 535 540
 Glu Leu Gln Leu Asp Trp Gln Lys Gln Lys Gly Gly Val Arg Arg Ala
 545 550 555 560
 Leu Phe Leu Ala Ser Arg Gln Ala Thr Leu Thr Gln Thr Leu Leu Ile
 565 570 575
 Gln Asn Gly Ala Arg Glu Asp Cys Arg Glu Met Lys Ile Tyr Leu Arg
 580 585 590
 Asn Glu Ser Glu Phe Arg Asp Lys Leu Ser Pro Ile His Ile Ala Leu
 595 600 605
 Asn Phe Ser Leu Asp Pro Gln Ala Pro Val Asp Ser His Gly Leu Arg
 610 615 620
 Pro Ala Leu His Tyr Gln Ser Lys Ser Arg Ile Glu Asp Lys Ala Gln
 625 630 635 640
 Ile Leu Leu Asp Cys Gly Glu Asp Asn Ile Cys Val Pro Asp Leu Gln
 645 650 655
 Leu Glu Val Phe Gly Glu Gln Asn His Val Tyr Leu Gly Asp Lys Asn
 660 665 670
 Ala Leu Asn Leu Thr Phe His Ala Gln Asn Val Gly Glu Gly Gly Ala
 675 680 685
 Tyr Glu Ala Glu Leu Arg Val Thr Ala Pro Pro Glu Ala Glu Tyr Ser
 690 695 700
 Gly Leu Val Arg His Pro Gly Asn Phe Ser Ser Leu Ser Cys Asp Tyr
 705 710 715 720

Phe Ala Val Asn Gln Ser Arg Leu Leu Val Cys Asp Leu Gly Asn Pro
725 730 735
Met Lys Ala Gly Ala Ser Leu Trp Gly Gly Leu Arg Phe Thr Val Pro
740 745 750
His Leu Arg Asp Thr Lys Lys Thr Ile Gln Phe Asp Phe Gln Ile Leu
755 760 765
Ser Lys Asn Leu Asn Asn Ser Gln Ser Asp Val Val Ser Phe Arg Leu
770 775 780
Ser Val Glu Ala Gln Ala Gln Val Thr Leu Asn Gly Val Ser Lys Pro
785 790 795 800
Glu Ala Val Leu Phe Pro Val Ser Asp Trp His Pro Arg Asp Gln Pro
805 810 815
Gln Lys Glu Glu Asp Leu Gly Pro Ala Val His His Val Tyr Glu Leu
820 825 830
Ile Asn Gln Gly Pro Ser Ser Ile Ser Gln Gly Val Leu Glu Leu Ser
835 840 845
Cys Pro Gln Ala Leu Glu Gly Gln Gln Leu Leu Tyr Val Thr Arg Val
850 855 860
Thr Gly Leu Asn Cys Thr Thr Asn His Pro Ile Asn Pro Lys Gly Leu
865 870 875 880
Glu Leu Asp Pro Glu Gly Ser Leu His His Gln Gln Lys Arg Glu Ala
885 890 895
Pro Ser Arg Ser Ser Ala Ser Ser Gly Pro Gln Ile Leu Lys Cys Pro
900 905 910
Glu Ala Glu Cys Phe Arg Leu Arg Cys Glu Leu Gly Pro Leu His Gln
915 920 925
Gln Glu Ser Gln Ser Leu Gln Leu His Phe Arg Val Trp Ala Lys Thr
930 935 940
Phe Leu Gln Arg Glu His Gln Pro Phe Ser Leu Gln Cys Glu Ala Val
945 950 955 960
Tyr Lys Ala Leu Lys Met Pro Tyr Arg Ile Leu Pro Arg Gln Leu Pro
965 970 975

Gln Lys Glu Arg Gln Val Ala Thr Ala Val Gln Trp Thr Lys Ala Glu
 980 985 990

Gly Ser Tyr Gly Val Pro Leu Trp Ile Ile Ile Leu Ala Ile Leu Phe
 995 1000 1005

Gly Leu Leu Leu Leu Gly Leu Leu Ile Tyr Ile Leu Tyr Lys Leu Gly
 1010 1015 1020

Phe Phe Lys Arg Ser Leu Pro Tyr Gly Thr Ala Met Glu Lys Ala Gln
 1025 1030 1035 1040

Leu Lys Pro Pro Ala Thr Ser Asp Ala
 1045

<210> 19

<211> 1713

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1613)

<223> "n" at position 1613 can be any base.

<400> 19

aaggccctgc cagcttgga ggaattgtc cctgcctgct tctggagaaa gaagatattg 60
 acaccatcta cgggcaccat ggaactgctt caagtgacca ttctttttct tctgcccagt 120
 atttgcagca gtaacagcac aggtgtttta gaggcagcta ataattcact tgttgttact 180
 acaacaaaac catctataac aacaccaaac acagaatcat tacagaaaaa tgttgtcaca 240
 ccaacaactg gaacaactcc taaaggaaca atcaccaatg aattacttaa aatgtctctg 300
 atgtcaacag ctactttttt aacaagtaaa gatgaaggat tgaaagccac aaccactgat 360
 gtcaggaaga atgactccat catttcaaac gtaacagtaa caagtgttac acttcccaat 420
 gctgtttcaa cattacaaag ttccaaaccc aagactgaaa ctacagagttc aattaaaaca 480
 acagaaatac caggtagtgt tctacaacca gatgcatcac cttctaaaac tgggtacatta 540
 acctcaatac cagttacaat tccagaaaac acctcacagt ctcaagtaat agrcactgag 600
 ggtggaaaaa atgcaagcac ttcagcaacc agccggtctt attccagtat tattttgccg 660
 gtggttattg ctttgattgt aataacactt tcagtatttg ttctgggtggg tttgtaccga 720
 atgtgctgga aggcagatcc gggcacacca gaaaatggaa atgatcaacc tcagtctgat 780
 aaagagagcg tgaagcttct taccgttaag acaatttctc atgagtctgg tgagcactct 840
 gcacaaggaa aaaccaagaa ctgacagctt gaggaattct ctccacacct aggcaataat 900
 tacgtttaat cttcagcttc tatgcaccaa gcgtggaaaa ggagaaagtc ctgcagaatc 960
 aatcccagact tccataacct ctgctggact gtaccagacg tctgtcccag taaagtgatg 1020
 tccagctgac atgcaataat ttgatggaat caaaaagaac cccggggctc tcctgttctc 1080
 tcacatttaa aaattccatt actccattta caggagcggt cctaggaaaa ggaatttttag 1140
 gaggagaatt tgtgagcagt gaatctgaca gccagaggag tgggctcgct gataggcatg 1200

actttcctta atgtttaaag ttttccgggc caagaatttt tatccatgaa gactttccta 1260
cttttctcgg tgttcttata ttacctactg ttagtattta ttgtttacca ctatgttaat 1320
gcagggaaaaa gttgcacgtg tattattaaa tattaggtag aaatcatacc atgctacttt 1380
gtacatataa gtattttatt cctgctttcg tgttactttt aataaataac tactgtactc 1440
aatactctaa aaatactata acatgactgt gaaaatggca atgttattgt cttcctataa 1500
ttatgaatat ttttggatgg attattagaa tacatgaact cactaatgaa aggcatttgt 1560
aataagtcag aaagggacat aggattcaca tatcagactg ttagggggag agntaattat 1620
cagttctttg gtctttctat ttgtcattca tactatgtga tgaagatgta agtgcaaggg 1680
catttataac actatactgc attcattaga tat 1713

<210> 20

<211> 261

<212> PRT

<213> Homo sapiens

<220>

<221> UNSURE

<222> (172)

<223> "Xaa" at position 172 can be any amino acid.

<400> 20

Met Glu Leu Leu Gln Val Thr Ile Leu Phe Leu Leu Pro Ser Ile Cys
1 5 10 15

Ser Ser Asn Ser Thr Gly Val Leu Glu Ala Ala Asn Asn Ser Leu Val
20 25 30

Val Thr Thr Thr Lys Pro Ser Ile Thr Thr Pro Asn Thr Glu Ser Leu
35 40 45

Gln Lys Asn Val Val Thr Pro Thr Thr Gly Thr Thr Pro Lys Gly Thr
50 55 60

Ile Thr Asn Glu Leu Leu Lys Met Ser Leu Met Ser Thr Ala Thr Phe
65 70 75 80

Leu Thr Ser Lys Asp Glu Gly Leu Lys Ala Thr Thr Thr Asp Val Arg
85 90 95

Lys Asn Asp Ser Ile Ile Ser Asn Val Thr Val Thr Ser Val Thr Leu
100 105 110

Pro Asn Ala Val Ser Thr Leu Gln Ser Ser Lys Pro Lys Thr Glu Thr
115 120 125

Gln Ser Ser Ile Lys Thr Thr Glu Ile Pro Gly Ser Val Leu Gln Pro
130 135 140

Asp Ala Ser Pro Ser Lys Thr Gly Thr Leu Thr Ser Ile Pro Val Thr
 145 150 155 160

Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Xaa Thr Glu Gly Gly
 165 170 175

Lys Asn Ala Ser Thr Ser Ala Thr Ser Arg Ser Tyr Ser Ser Ile Ile
 180 185 190

Leu Pro Val Val Ile Ala Leu Ile Val Ile Thr Leu Ser Val Phe Val
 195 200 205

Leu Val Gly Leu Tyr Arg Met Cys Trp Lys Ala Asp Pro Gly Thr Pro
 210 215 220

Glu Asn Gly Asn Asp Gln Pro Gln Ser Asp Lys Glu Ser Val Lys Leu
 225 230 235 240

Leu Thr Val Lys Thr Ile Ser His Glu Ser Gly Glu His Ser Ala Gln
 245 250 255

Gly Lys Thr Lys Asn
 260

<210> 21
 <211> 1434
 <212> DNA
 <213> Homo sapiens

<400> 21
 atgcatcttg cattccttgt gctgttgtgt ctgccagtct gctctgccta tcctctgagt 60
 ggggcagcaa aagaggagga ctccaacaag gatcttgccc agcaatacct agaaaagtac 120
 tacaacctcg aaaaggatgt gaaacagttt agaagaaagg acagtaatct cattgttaaa 180
 aaaatccaag gaatgcagaa gttccttggg ttggagggtga cagggaagct agacactgac 240
 actctggagg tgatgcgcaa gcccagggtg ggagttcctg acgttgggtca cttcagctcc 300
 tttcctggca tgccgaagtg gaggaaaacc caccttacat acaggattgt gaattataca 360
 ccagatttgc caagagatgc tgttgattct gccattgaga aagctctgaa agtctgggaa 420
 gaggtgactc cactcacatt ctccaggctg tatgaaggag aggctgatat aatgatctct 480
 ttgcagatta aagaacatgg agacttttac tcttttgatg gccaggaca cagtttggct 540
 catgcctacc cacctggacc tgggctttat ggagatattc actttgatga tgatgaaaaa 600
 tggacagaag atgcatcagg caccaattta ttcctcgttg ctgctcatga acttggccac 660
 tccttggggc tctttcactc agccaacact gaagctttga tgtaccact ctacaactca 720
 ttcacagagc tcgccaggtt ccgcctttcg caagatgatg tgaatggcat tcagtctctc 780
 tacggacctc cccctgcctc tactgaggaa cccctggtgc ccacaaaatc tgttccttcg 840
 ggatctgaga tgccagccaa gtgtgatcct gctttgtcct tcgatgccat cagcactctg 900
 aggggagaat atctgttctt taaagacaga tatttttggc gaagatcca ctggaaccct 960

gaacctgaat ttcatttgat ttctgcattt tggccctctc ttccatcata tttggatgct 1020
 gcatatgaag ttaacagcag ggacaccgtt tttattttta aaggaaatga gttctgggccc 1080
 atcagaggaa atgaggtaca agcaggttat ccaagaggca tccataccct gggttttcct 1140
 ccaaccataa ggaaaattga tgcagctggt tctgacaagg aaaagaagaa aacatacttc 1200
 tttgcagcgg acaaatactg gagatttgat gaaaatagcc agtccatgga gcaaggcttc 1260
 cctagactaa tagctgatga ctttccagga gttgagccta aggttgatgc tgtattacag 1320
 gcatttggat ttttctactt cttcagtgga tcatcacagt ttgagtttga ccccaatgcc 1380
 aggatggtga cacacatatt aaagagtaac agctgggttac attgctctag atag 1434

<210> 22

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (3)

<223> The xaa at position 3 represents any amino acid.

<220>

<223> Description of Artificial Sequence: cytokine
 receptor extracellular motif found in many species

<400> 22

Trp Ser Xaa Trp Ser

1

5



PAGE:

1

ERROR LISTING
PATENT APPLICATION

DATE: 12/19/2000
TIME: 17:26:36

INPUT SEQ: P:\PatIn2\A68110-1\A68110-1.app

L:775 M:341 W: "n" or "Xaa" used, for SEQ ID#:19
L:821 M:341 W: "n" or "Xaa" used, for SEQ ID#:20
L:890 M:341 W: "n" or "Xaa" used, for SEQ ID#:22

PAGE:

1

VERIFICATION SUMMARY REPORT
PATENT APPLICATION

DATE: 12/19/2000
TIME: 17:26:36

INPUT SEQ PatIn2\A68110-1\A68110-1.app

GENERAL INFORMATION SECTION

3,<110> MURRAY, RICHARD
5,<120> Novel Methods of Diagnosis of Angiogenesis,
6, Compositions, and Methods of Screening for Angiogenesis
7, Modulators
9,<130> A-68110-1/DJB/RMS/DCF
11,<140> US 09/637,977
12,<141> 2000-08-11
14,<150> US 60/148,425
15,<151> 1999-08-11
17,<160> 22
19,<170> PatentIn Ver. 2.1

ERRORED LINES SECTION

W--> 775 aataagtcag aaagggacat aggattcaca tatcagactg ttagggggag agntaattat 1620
W--> 821 Ile Pro Glu Asn Thr Ser Gln Ser Gln Val Ile Xaa Thr Glu Gly Gly
W--> 890 Trp Ser Xaa Trp Ser

STATISTICS SUMMARY

Application Serial Number: US 09/637,977A
Alpha or Numeric: Numeric
Application Class:
Application File Date: 2000-08-11
Art Unit:
Software Application: PatentIn
Total Number of Sequences: 22
Number of Errors: 0
Number of Warnings: 3
Number of Corrections: 0